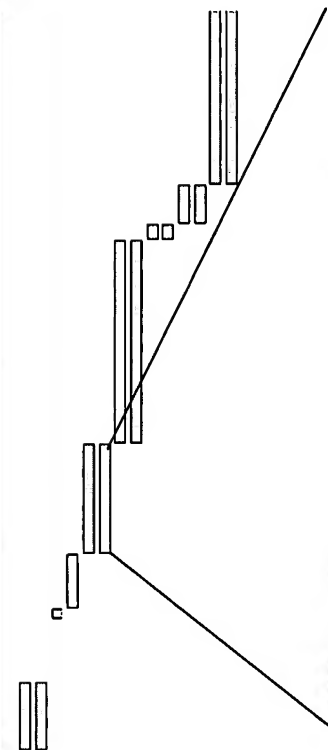
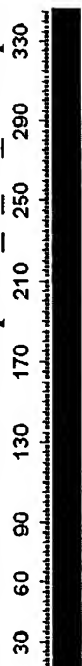




Sample 1: Heteroplasmy (mixture of lengths) is detrimental to sequencing approaches but does not adversely affect MS measurements

HV1-1-outer-variant1: p482_3_26_2003.pek, scan HV1-1-outer-variant2: p482_3_26_2003.pek, scan 1



Scan number: 1
Position: 94 to 145
Length: 52
Number of matched peaks: 1
Fragment seq: AATAAAACCAATCCACATCAAAACCCCCCATGCTTACAAGCAAGT
Average Predicted fragment mass: 15753.66286 ± 0.00000 daltons
Average matched peak mass: 15753.63000 ± 0.00000 daltons
Total peak abundance: 4.01E+06
Average peak abundance: 4.01E+06
Maximum peak abundance: 4.01E+06
Weighted average match error: 2.07327 ± 0.00000 ppm
Raw average match error: 2.07327 ± 0.00000 ppm
Weighted average peak fit: 0.05900 ± 0.00000
No ambiguous assignments in group

(opposite strand also observed)

HV1-1-outer-variant1
HV1-1-outer-variant2

acataaaaaaaccaatccacatcaaaacccccccccccatgcttacaagcaagt
aataaaaaaaccaatccacatcaaaacccccccccccatgcttacaagcaagt

(SEQ ID NO: 44)
(SEQ ID NO: 45)

Heteroplasmy region

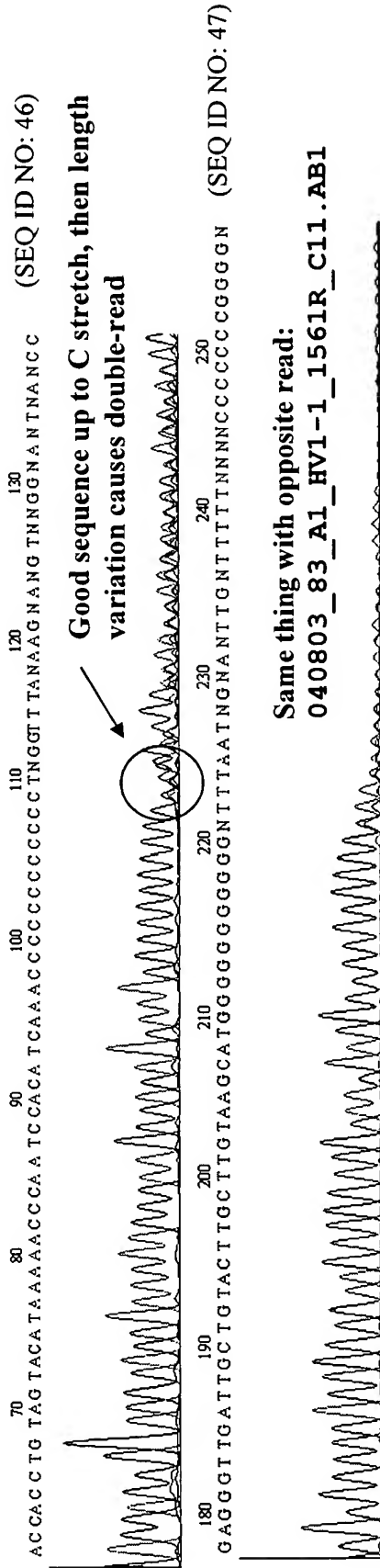
Figure 20A



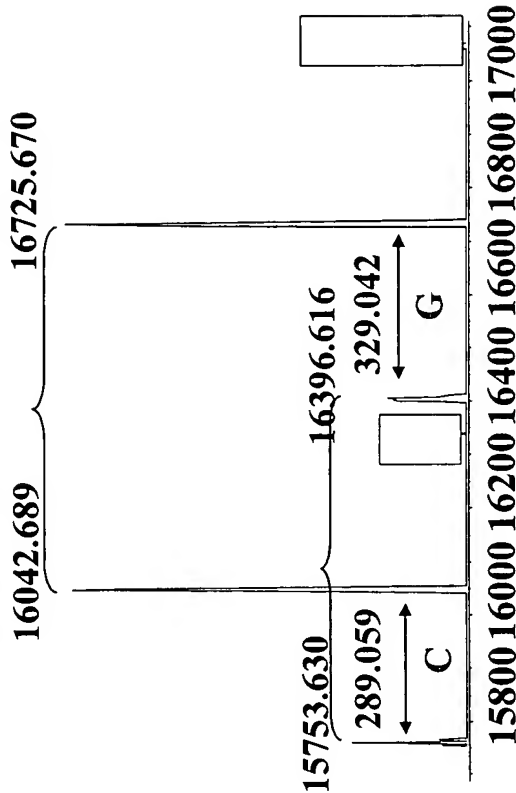
"Replacement Sheet" } **Figure 20B**

MS Approach Succeeds Where Conventional Sequencing Fails

Sequences differ in length by one base in the 'C' stretch. Both variants appear in digest data. Sequencing profile also points to a length variation in this region: Example trace: 040803_81_A1_HV1-1_1560F_A11.AB1



Same thing with opposite read:
040803_83_A1_HV1-1_1561R_C11.AB1



MS detects multiple species simultaneously while sequencing requires pure sample for maximum information content

Ratio of short to long alleles is 1:3